

SEQUENCE LISTING

<110> BRAIN BIOTECHNOLOGY RESEARCH AND INFORMATION NETWORK AG
 Verseck, Stefan
 Liebeton, Klaus
 Eck, Jurgen

<120> Nitrile hydratases from metagenome libraries

<130> 009848-0356700

<140> 10/593,357
 <141> 2006-09-18

<150> WO PCT/EP2005/002556
 <151> 2005-03-10

<150> DE 10 2004 013 842.7
 <151> 2004-03-20

<160> 86

<170> PatentIn version 3.1

<210> 1
 <211> 12
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer

<400> 1
 gcsmrsgcst gg 12

<210> 2
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 2
 ggsctscsc c 11

<210> 3
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 3
 ggsagsagc c 11

<210> 4
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<400> 4
ggncgcwbsg g 11

<210> 5
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or c

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 5
gCnmrrgcnt gg 12

<210> 6
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (6)..(6)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 6
ggnytnccnc c 11

<210> 7
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> a or g or c or t/u

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> a or g or c or t/u

<400> 7
 ggnggnarnc c 11

<210> 8
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<400> 8
 gwngwrtccc a 11

<210> 9
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> a or g or c or t/u

<400> 9
 gcntggryng a 11

<210> 10
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> a or g or c or t/u

<400> 10
 ggnytsccnc c 11

<210> 11
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> a or g or c or t/u

<400> 11
 ggnggsarnc c 11

<210> 12
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or g or c or t/u

<400> 12
 swnswrtccc a 11

<210> 13	
<211> 12	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 13	
gccaaggtcg tc	12
<210> 14	
<211> 11	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 14	
ggccggtcct g	11
<210> 15	
<211> 15	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 15	
tccttgtagc aggtc	15
<210> 16	
<211> 7	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 16	
gcccgcc	7
<210> 17	
<211> 15	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 17	
ggcgctaaag ttgtt	15
<210> 18	
<211> 12	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 18	
tggccggttc tg	12

<210> 19	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 19	
caaattcttt ataccaagtc	20
<210> 20	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 20	
ccatataatcg catttcagct	20
<210> 21	
<211> 13	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 21	
ggtcgtggcc aag	13
<210> 22	
<211> 11	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 22	
ggccggtcct g	11
<210> 23	
<211> 15	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 23	
tccttgtagc aggtc	15
<210> 24	
<211> 13	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 24	
gcgcatttcg gcg	13

<210> 25	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 25	
gcccaaggctcg tcgcsmrsgc stgg	24
<210> 26	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 26	
ggccggtcct gggscstscs cc	22
<210> 27	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 27	
tccttgtagc aggtcggsgg sagscc	26
<210> 28	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<220>	
<221> misc_feature	
<222> (10)..(10)	
<223> a or c or g or t/u	
<400> 28	
gcccgccggn cgcwbsgg	18
<210> 29	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<220>	
<221> misc_feature	
<222> (18)..(18)	
<223> a or c or g or t/u	

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> a or c or g or t/u

<400> 29
 ggcgctaaag ttgttgcnmr rgcntgg

27

<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> a or c or g or t/u

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> a or c or g or t/u

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> a or c or g or t/u

<400> 30
 tggccggttc tgggnytncc nc

22

<210> 31
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (23)..(23)
 <223> a or c or g or t/u

<220>
 <221> misc_feature
 <222> (26)..(26)
 <223> a or c or g or t/u

<220>
 <221> misc_feature
 <222> (29)..(29)
 <223> a or c or g or t/u

<400> 31
 caaatcttt ataccaagtc ggnggnarnc c

31

<210> 32
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (23)..(23)
 <223> a or c or g or t/u

<400> 32
 ccatatatcg catttcagct gwngrwtccc a

31

<210> 33
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> a or c or g or t/u

<220>
 <221> misc_feature
 <222> (22)..(22)
 <223> a or c or g or t/u

<400> 33
 ggctcgtggcc aaggcntggr ynga

24

<210> 34
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (14)..(14)
 <223> a or c or g or t/u

<220>
 <221> misc_feature
 <222> (20)..(20)
 <223> a or c or g or t/u

<400> 34
 ggccggtcct gggnytsccn cc

22

<210> 35
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <220>
 <221> misc_feature
 <222> (18)..(18)
 <223> a or c or g or t/u

 <220>
 <221> misc_feature
 <222> (24)..(24)
 <223> a or c or g or t/u

 <400> 35
 tccttgtagc aggtcggngg sarncc 26

 <210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <220>
 <221> misc_feature
 <222> (16)..(16)
 <223> a or c or g or t/u

 <400> 36
 gcgcatttcg gcgswns wrt ccca 24

 <210> 37
 <211> 705
 <212> DNA
 <213> Unknown

 <220>
 <223> Metagenome - alpha unit nitrile hydratase - M6aH6

 <220>
 <221> CDS
 <222> (1)..(705)

 <400> 37

 atg agc aag cac gta cac gat tac tac gcg aag aag aag cac gac cac 48
 Met Ser Lys His Val His Asp Tyr Tyr Ala Lys Lys Lys His Asp His
 1 5 10 15

 gat cat gac cac gac gtc cac gag gcg atc gag gac cgg gac gag ggt 96
 Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly
 20 25 30

 ccg ccg tcg gaa ttc gag atc atg agc cgc gcc atg cag gag ctg ctg 144
 Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu
 35 40 45

gaa gag aag ggc gtc gtc acc gcg gag cag gtc cgg cgc agc atg gag Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu 50 55 60	192
aag ttc gag gaa gag ctg ccc tac cgg ggg gcg cgg gtc gtc gcg cac Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His 65 70 75 80	240
gcc tgg acc gac ccg gaa ttc aag aag cgg ctg ctg gcg gac ggc aag Ala Trp Thr Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Lys 85 90 95	288
gcc gcc gtc tcg gag ttc ggc atc gat ttg gaa gcc gag cgg ctg atc Ala Ala Val Ser Glu Phe Gly Ile Asp Leu Glu Ala Glu Arg Leu Ile 100 105 110	336
gcg gtc gcg aac aca acg gac gtg cac aac gtc atc gtg tgc acg ctg Ala Val Ala Asn Thr Thr Asp Val His Asn Val Ile Val Cys Thr Leu 115 120 125	384
tgc tcg tgc tac ccg cgc acg ctg ctc ggc atg ccg ccg acc tgg tac Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr 130 135 140	432
aag agc gat aac tac cgc tcg cgc gtg gtc tac gaa ccg cgc gcg gtg Lys Ser Asp Asn Tyr Arg Ser Arg Val Val Tyr Glu Pro Arg Ala Val 145 150 155 160	480
ctg aag gaa ttc ggc acc gtg ctg ccg gag cgc gtc acc gtg cgc gtg Leu Lys Glu Phe Gly Thr Val Leu Pro Glu Arg Val Thr Val Arg Val 165 170 175	528
cac gac tcc aac gcc gac atg cgc tac gtg gtg atc ccc atg cgc ccg His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro 180 185 190	576
cag gga acc gag ggc tgg agc gag gag cgg ctc gcg gag ctg ctg acg Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr 195 200 205	624
cgc gac acg ctg gtg ggg gtc acc gtg cca aaa gtg gaa gtc gga agt Arg Asp Thr Leu Val Gly Val Thr Val Pro Lys Val Glu Val Gly Ser 210 215 220	672
cga aag tcg aaa ggc gga agt aaa acc cgc tag Arg Lys Ser Lys Gly Gly Ser Lys Thr Arg 225 230	705

<210> 38
 <211> 234
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M6aH6
 <400> 38

Met Ser Lys His Val His Asp Tyr Tyr Ala Lys Lys Lys His Asp His 1 5 10 15
Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly 20 25 30
Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu 35 40 45

Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu
 50 55 60
 Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His
 65 70 75 80
 Ala Trp Thr Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Lys
 85 90 95
 Ala Ala Val Ser Glu Phe Gly Ile Asp Leu Glu Ala Glu Arg Leu Ile
 100 105 110
 Ala Val Ala Asn Thr Thr Asp Val His Asn Val Ile Val Cys Thr Leu
 115 120 125
 Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr
 130 135 140
 Lys Ser Asp Asn Tyr Arg Ser Arg Val Val Tyr Glu Pro Arg Ala Val
 145 150 155 160
 Leu Lys Glu Phe Gly Thr Val Leu Pro Glu Arg Val Thr Val Arg Val
 165 170 175
 His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro
 180 185 190
 Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr
 195 200 205
 Arg Asp Thr Leu Val Gly Val Thr Val Pro Lys Val Glu Val Gly Ser
 210 215 220
 Arg Lys Ser Lys Gly Gly Ser Lys Thr Arg
 225 230

<210> 39
 <211> 657
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M12K24
 <220>
 <221> CDS
 <222> (1)..(657)

<400> 39

atg tcg gac gga aca aca att gga atc cag gcc gcg aca acc ctt cga	48
Met Ser Asp Gly Thr Thr Ile Gly Ile Gln Ala Ala Thr Thr Leu Arg	
1 5 10 15	
tca gcc atg aac att cca gct cgt gaa ttc gcc ctc cag cgc act gcg	96
Ser Ala Met Asn Ile Pro Ala Arg Glu Phe Ala Leu Gln Arg Thr Ala	
20 25 30	

ccg gtc gag cag cgt gtc gac gcg atc cag gcg gcg ctc gac gaa cgc Pro Val Glu Gln Arg Val Asp Ala Ile Gln Ala Ala Leu Asp Glu Arg 35 40 45	144
ggt ttg aac gcc agt gac gca gtc cag gaa ttg agc cac ctg gcg gag Gly Leu Asn Ala Ser Asp Ala Val Gln Glu Leu Ser His Leu Ala Glu 50 55 60	192
gag caa tgg att ccg cgc aat ggc gcg cgg gtc gtc gcc aaa gcc tgg Glu Gln Trp Ile Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala Trp 65 70 75 80	240
gtc gac ccg gaa ttc cgc gcg cgg ctt ctg gcc gac ggt cgc gcc gcc Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala 85 90 95	288
gtt gcc gaa ctg ggc ctc tcg atg ccg aag cat cac cgg cac ctc gtg Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val 100 105 110	336
gtg ctg gag aac acg ccg agc gtg cag aac gtc atc tgc tgc acg cag Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln 115 120 125	384
tgc tcg tgc acg gcg ttc acg atc atc gga ctg ccg ccc gac tgg tac Cys Ser Cys Thr Ala Phe Thr Ile Ile Gly Leu Pro Pro Asp Trp Tyr 130 135 140	432
aag gac ctg gaa tac cgc gcg cga gtc gtc cgg gag tcg cgc acc gtg Lys Asp Leu Glu Tyr Arg Ala Arg Val Val Arg Glu Ser Arg Thr Val 145 150 155 160	480
ctg aag gag atg gga ctg gat ctg cct cgg gat gtc gaa att cgc gtc Leu Lys Glu Met Gly Leu Asp Leu Pro Arg Asp Val Glu Ile Arg Val 165 170 175	528
tgg gat acc act gcc gac acg cgc tac atg gta ttg ccg gta cag ccg Trp Asp Thr Thr Ala Asp Thr Arg Tyr Met Val Leu Pro Val Gln Pro 180 185 190	576
ccg gaa acc atc ggc tgg ccc gag gag aaa ctg gtc gac atc gtg acg Pro Glu Thr Ile Gly Trp Pro Glu Glu Lys Leu Val Asp Ile Val Thr 195 200 205	624
cgc gac ggc atg atc ggc gtc gcg cgg gta tag Arg Asp Gly Met Ile Gly Val Ala Arg Val 210 215	657

<210> 40

<211> 218

<212> PRT

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M12K24

<400> 40

Met Ser Asp Gly Thr Thr Ile Gly Ile Gln Ala Ala Thr Thr Leu Arg 1 5 10 15
--

Ser Ala Met Asn Ile Pro Ala Arg Glu Phe Ala Leu Gln Arg Thr Ala 20 25 30

Pro Val Glu Gln Arg Val Asp Ala Ile Gln Ala Ala Leu Asp Glu Arg 35 40 45

Gly Leu Asn Ala Ser Asp Ala Val Gln Glu Leu Ser His Leu Ala Glu
 50 55 60
 Glu Gln Trp Ile Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala Trp
 65 70 75 80
 Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala
 85 90 95
 Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val
 100 105 110
 Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln
 115 120 125
 Cys Ser Cys Thr Ala Phe Thr Ile Ile Gly Leu Pro Pro Asp Trp Tyr
 130 135 140
 Lys Asp Leu Glu Tyr Arg Ala Arg Val Val Arg Glu Ser Arg Thr Val
 145 150 155 160
 Leu Lys Glu Met Gly Leu Asp Leu Pro Arg Asp Val Glu Ile Arg Val
 165 170 175
 Trp Asp Thr Thr Ala Asp Thr Arg Tyr Met Val Leu Pro Val Gln Pro
 180 185 190
 Pro Glu Thr Ile Gly Trp Pro Glu Glu Lys Leu Val Asp Ile Val Thr
 195 200 205
 Arg Asp Gly Met Ile Gly Val Ala Arg Val
 210 215

<210> 41
 <211> 699
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M29M24

<220>
 <221> CDS
 <222> (1)..(699)

<400> 41

atg gag acg aca cgc cgc ggc ttc ttg aag aaa gcc ggg acc gcc gcc	48
Met Glu Thr Thr Arg Arg Gly Phe Leu Lys Lys Ala Gly Thr Ala Ala	
1 5 10 15	
ggt gcg acg gct gca ccc gtt gga ctc gcc aag atc gct cac tcc cac	96
Gly Ala Thr Ala Ala Pro Val Gly Leu Ala Lys Ile Ala His Ser His	
20 25 30	
gag cac cag gcc gtt cct tcc gac ctc acg ctc cgg gtc aag tcc ctc	144
Glu His Gln Ala Val Pro Ser Asp Leu Thr Leu Arg Val Lys Ser Leu	
35 40 45	

gaa tgc ctg ctg gtc gag aag ggt ctc gtg gac cgt gag gcc ctc gac Glu Ser Leu Leu Val Glu Lys Gly Leu Val Asp Arg Glu Ala Leu Asp 50 55 60	192
gtg ctc gtc gat acc tac gag aac aag atc ggt ccg cga aac ggc gct Val Leu Val Asp Thr Tyr Glu Asn Lys Ile Gly Pro Arg Asn Gly Ala 65 70 75 80	240
cgc gtc gtc gcg cgg gcg tgg gtc gat ccc gcg tac aaa gag cgc ctg Arg Val Val Ala Arg Ala Trp Val Asp Pro Ala Tyr Lys Glu Arg Leu 85 90 95	288
ctg aaa gac gcc acc tgc gcg atc gcc gag ctc ggt tac acc gga gcc Leu Lys Asp Ala Thr Ser Ala Ile Ala Glu Leu Gly Tyr Thr Gly Ala 100 105 110	336
cag ggt gag cac atg gtg gcg ctc gag aat acc ccc gcg gtg cac aac Gln Gly Glu His Met Val Ala Leu Glu Asn Thr Pro Ala Val His Asn 115 120 125	384
ctc gtc gtt tgc acg ctc tgc tcc tgc tat cca tgg ccg gtg ctc ggt Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly 130 135 140	432
ctg ccc ccg gtc tgg tac aaa tgc gcg ccc tac cga tcg cgc tcg gtc Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Ser Val 145 150 155 160	480
atc gat ccg cgc ggc gtt ctc ggc gag ttc ggg ctc gag ctg ccg gaa Ile Asp Pro Arg Gly Val Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu 165 170 175	528
ggg gtc gag gtg cgc gtc tgg gac tcg acg gcg gag ctc ccg tat ctc Gly Val Glu Val Arg Val Trp Asp Ser Thr Ala Glu Leu Arg Tyr Leu 180 185 190	576
gtt ttg ccg gag cgg ccc gaa ggc acg gcg caa ctg agc gaa gaa gcg Val Leu Pro Glu Arg Pro Glu Gly Thr Ala Gln Leu Ser Glu Glu Ala 195 200 205	624
ctc gcg gat ctc gtc acc cgg gat gcc atg atc ggc gtc gcg aaa gtc Leu Ala Asp Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val 210 215 220	672
tcg ttg ccc gcg ggc ggc gcc gaa tga Ser Leu Pro Ala Gly Gly Ala Glu 225 230	699

<210> 42
 <211> 232
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M29M24

<400> 42

Met Glu Thr Thr Arg Arg Gly Phe Leu Lys Lys Ala Gly Thr Ala Ala
 1 5 10 15

Gly Ala Thr Ala Ala Pro Val Gly Leu Ala Lys Ile Ala His Ser His
 20 25 30

Glu His Gln Ala Val Pro Ser Asp Leu Thr Leu Arg Val Lys Ser Leu
 35 40 45

Glu Ser Leu Leu Val Glu Lys Gly Leu Val Asp Arg Glu Ala Leu Asp
 50 55 60
 Val Leu Val Asp Thr Tyr Glu Asn Lys Ile Gly Pro Arg Asn Gly Ala
 65 70 75 80
 Arg Val Val Ala Arg Ala Trp Val Asp Pro Ala Tyr Lys Glu Arg Leu
 85 90 95
 Leu Lys Asp Ala Thr Ser Ala Ile Ala Glu Leu Gly Tyr Thr Gly Ala
 100 105 110
 Gln Gly Glu His Met Val Ala Leu Glu Asn Thr Pro Ala Val His Asn
 115 120 125
 Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
 130 135 140
 Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Ser Val
 145 150 155 160
 Ile Asp Pro Arg Gly Val Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu
 165 170 175
 Gly Val Glu Val Arg Val Trp Asp Ser Thr Ala Glu Leu Arg Tyr Leu
 180 185 190
 Val Leu Pro Glu Arg Pro Glu Gly Thr Ala Gln Leu Ser Glu Glu Ala
 195 200 205
 Leu Ala Asp Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
 210 215 220
 Ser Leu Pro Ala Gly Gly Ala Glu
 225 230

<210> 43
 <211> 639
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M2K17

<220>
 <221> CDS
 <222> (1)..(639)

<400> 43

atg cct gac gac cat gcc cat ccg gat gat cat gcg cat ggc tcg gaa	48
Met Pro Asp Asp His Ala His Pro Asp Asp His Ala His Gly Ser Glu	
1 5 10 15	
ttg tcc gag atg gat atc cgg gtg cgg gcg ctg gag acc atc ctg acc	96
Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr	
20 25 30	

gag aag ggc tat gtc gat ccg gcg gcg ctc gac cgg atc gtc gag gcg Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala 35 40 45	144
ttc gag acc agg atc ggc ccg cat atc ggc gcc cgt atc gtg gca cgg Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg 50 55 60	192
gct tgg gcc gac gcc gaa ttc aag cgg cgg ctg ctc gcc gac gcg acc Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr 65 70 75 80	240
gag gcg gcg aat tcg ctg ggt cat gcg agc ccg gtc ggc agc cat ctg Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu 85 90 95	288
atc gcg gtc gag aac acg ccg cag acc cac aac ctc gtc gtc tgc act Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr 100 105 110	336
ttg tgc tcg tgt tat ccg tgg gag gtg ctg gga ttg ccg ccg gtc tgg Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp 115 120 125	384
tac aaa tcc gct gcc tac cgc tcg cgc gtg gtg atc gac ccc aag ggc Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly 130 135 140	432
gtc ctc gcc gag ttc ggc ctg acc ctg cca ccg gag acc ggg atc cgc Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg 145 150 155 160	480
atc tgg gat tcg acc gcc gag acc cgg ttt ctg gtg gtg ccg atg cgg Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg 165 170 175	528
ccc ccc ggc acc gca ggc tgg agc gag gaa cgg ctc gcc gaa ctc gtc Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val 180 185 190	576
acc cgc gac agc atg atc ggc act ggt ctg gcc ggg gcg ccg cag gag Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu 195 200 205	624
atg gcc tcg gca tga Met Ala Ser Ala 210	639

<210> 44

<211> 212

<212> PRT

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M2K17

<400> 44

Met Pro Asp Asp His Ala His Pro Asp Asp His Ala His Gly Ser Glu
1 5 10 15

Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr
20 25 30

Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala
35 40 45

Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg
 50 55 60
 Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr
 65 70 75 80
 Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu
 85 90 95
 Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr
 100 105 110
 Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp
 115 120 125
 Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly
 130 135 140
 Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg
 145 150 155 160
 Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg
 165 170 175
 Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val
 180 185 190
 Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu
 195 200 205
 Met Ala Ser Ala
 210

<210> 45
 <211> 696
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M15aA6

<220>
 <221> CDS
 <222> (1)..(696)

<400> 45

atg cgt tcg ccc ggt gag gcc tca gca acg caa cca gcg ctc att cgg	48
Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg	
1 5 10 15	
ctg cat gat cga gct ggc ggc gtt cga tca ttg cgc ggc aaa agg tct	96
Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser	
20 25 30	
cat cgc gcc gga tcg cat cct cgg ggc gct cgc gca tcc gtc gcc aca	144
His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr	
35 40 45	

ggg tgg ttc gtt ccg ttc tcg gcc agg ctc gcc cgg aaa ggc atc gct Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala 50 55 60	192
cct ccg gcc gag atc gcc gag cgg atc gcc gtc acc gat cgc gca tca Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser 65 70 75 80	240
ccg gca atg ggc gct cgc atg gtc gcc aag gcc tgg acc gat ccc gcc Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala 85 90 95	288
ttc cgc acc ctg ctc ttg gaa gac gga acc cgc gcg gcg gaa tcg ctc Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu 100 105 110	336
ggc atc atg atg cgc ggc gcc ccg cct ctc ggt gtg ctg gag aat acg Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr 115 120 125	384
ccc gag att cat cac ctc gtc gtt tgc acg ctg tgc agt tgt tac ccg Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro 130 135 140	432
cgc gcg gtg ctg ggc tat ccg ccg ttc tgg ttc aaa tcc gcc gcc tac Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr 145 150 155 160	480
cgg gca cgt gcg gtg cgc gac ccg cgc ggt ctg atc gcc gaa tgg ggc Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly 165 170 175	528
acc atg ctg ccc gac gat gtc cgc gtg cga gtg gtg gac agt acg gcc Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala 180 185 190	576
gac tat cgc tgg atg gtt ctg ccg gtg cgg ccg gcc ggc act gcg ggc Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly 195 200 205	624
tgg gat gag gag cgc ctc gcc gca atc gta cgc gaa ggc gat atg atc Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile 210 215 220	672
ggg gtg acc atc cct cgt ctt taa Gly Val Thr Ile Pro Arg Leu 225 230	696

<210> 46

<211> 231

<212> PRT

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M15aA6

<400> 46

Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg 1 5 10 15
Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser 20 25 30
His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr 35 40 45

Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala
 50 55 60
 Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser
 65 70 75 80
 Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala
 85 90 95
 Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu
 100 105 110
 Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr
 115 120 125
 Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro
 130 135 140
 Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr
 145 150 155 160
 Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly
 165 170 175
 Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala
 180 185 190
 Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly
 195 200 205
 Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile
 210 215 220
 Gly Val Thr Ile Pro Arg Leu
 225 230

<210> 47
 <211> 576
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M23dA12

<220>
 <221> CDS
 <222> (1)..(576)

<400> 47

atg cag ttg cgc gtg cgg gcg ctg gaa acc gtt cta gcc gaa aag ggt	48
Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly	
1 5 10 15	
tat ctc gat ccc gcc gcg ctt gat gcg atg atc gaa gcc tac gag acg	96
Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr	
20 25 30	

cgg att ggg ccg cat aac ggc gcg cgc gtc gtc gcc aag gcc tgg tcc 144
 Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser
 35 40 45
 gac gcc gca ttc aag cga ggc ctg gtc gag gat ggc acc aag gcc gtg 192
 Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val
 50 55 60
 cag tcg ttc ggc gtg gtc aat cgc gtc ggc gat cac ctg atc ggc gtc 240
 Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val
 65 70 75 80
 gag aac acg ccc acg ctg cac aac atc atc gtg tgc acg ttg tgc tcc 288
 Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser
 85 90 95
 tgc tat ccg tgg gaa gtg ctc ggc ctg ccg ccg gtc tgg tac aaa tcg 336
 Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser
 100 105 110
 gcg ccc tac cgc tcg cgc gcg gtc aac gac ccg cgc ggg gta ctc gcc 384
 Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala
 115 120 125
 gat ttc ggc ctg aag ctg gcg ccg gat atg caa atc cgt gtc tgg gat 432
 Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp
 130 135 140
 tcg acc gcc gag acg cgc ttc atc gtg ttg ccg atg cgc ccg gcc gga 480
 Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly
 145 150 155 160
 acc gac ggc tgg agc gaa gaa aag ctc gcc gcg ctg gtg aca cgc gat 528
 Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp
 165 170 175
 tgc atg atc ggc acc ggc tta ccc aag caa ccc aac gag gtc acg taa 576
 Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr
 180 185 190

<210> 48

<211> 191

<212> PRT

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M23dA12

<400> 48

Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly
1 5 10 15

Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr
20 25 30

Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser
35 40 45

Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val
50 55 60

Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val
65 70 75 80

Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser
 85 90 95
 Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser
 100 105 110
 Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala
 115 120 125
 Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp
 130 135 140
 Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly
 145 150 155 160
 Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp
 165 170 175
 Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr
 180 185 190

<210> 49
 <211> 624
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M49bD9

<220>
 <221> cds
 <222> (1)..(624)

<400> 49

atg agc gag cac gat tcc ggc gaa agc cat cac cat ccg cag cca cta Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu 1 5 10 15	48
tcg cag gcg gca ttg cgc gcg aag gcg atc gaa tcg ctg ctg gtc gaa Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu 20 25 30	96
aag ggg ctg atc gcg acc gac gtg atc gat cgc gtg gta gca acg tac Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr 35 40 45	144
gag aaa gaa gtc ggg ccg ctc aac ggc gct aaa gtc gtc gcg cgg gcc Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala 50 55 60	192
tgg acc gat ccg gag tac cgc cgc aga ctg ctc aag aac ggc acg gcg Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala 65 70 75 80	240
gcg att gcc gag ctg gga ttc ggc ggc ttg cag ggc gaa cac atg atg Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met 85 90 95	288
gtc gtg gaa aac acg ccg tcc gta cat aac gtg atc tgt tgc acg cta Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu 100 105 110	336

tgc tca tgc tat ccg tgg ccg gtc ctg gga ctt ccg ccg agc tgg tac Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr 115 120 125	384
aag tcg ctg gcg tat cgt tcg cga atc gtg cgc gag ccg cgc gcc gtc Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val 130 135 140	432
ctc ggc gaa ttc ggc ctc gaa ttg ccc gaa acg gtg gaa gtc cgc gta Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val 145 150 155 160	480
tgg gat agc agt gct gag atg cgc tat ctc gtg ttg ccg gag cgt cca Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro 165 170 175	528
gcg gga acg acg gag ttg agc gaa gcg gaa ttg gct tca ttg atc acg Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr 180 185 190	576
cgc gat gcc ttg atc ggc gtg gcg aaa gtc gcg gcg cca agc cgc tag Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg 195 200 205	624

<210> 50
<211> 207
<212> PRT
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M49bD9
<400> 50

Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu 1 5 10 15
Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu 20 25 30
Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr 35 40 45
Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala 50 55 60
Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala 65 70 75 80
Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met 85 90 95
Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu 100 105 110
Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr 115 120 125
Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val 130 135 140

Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val
145 150 155 160

Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro
165 170 175

Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr
180 185 190

Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg
195 200 205

<210> 51
<211> 600
<212> DNA
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M6dE2

<220>
<221> CDS
<222> (1)..(600)

<400> 51

atg agc aac cca cgc cgt cga gaa cgg tcg gcc cca ccg gat gcg cga Met Ser Asn Pro Arg Arg Glu Arg Ser 10 Ala Pro Pro Asp Ala Arg 1 5	48
gcc aag gcg ctc gca gaa gcg ctt tcg aag caa gga ctc gtg ccg gaa Ala Lys Ala Leu Ala Glu Ala Leu Ser 25 Lys Gln Gly Leu Val Pro Glu 20 30	96
ggg ttc ctc gac cag gtc ggt tct cac gcc gcg gag gcg tgg agc ccg Gly Phe Leu Asp Gln Val Gly Ser 40 His Ala Ala Glu Ala Trp Ser Pro 35 45	144
cga aac ggc gca cgg gtc gtg gcg cgg gcg tgg gtg gat ccc gag tac Arg Asn Gly Ala Arg Val Val 55 Ala Arg Ala Trp Val 60 Asp Pro Glu Tyr 50	192
cgg acg cgc ttg ctc gcc gac ggc acc gcc gcg tgc gcc gcg ctc ggc Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala 75 Cys Ala Ala Leu Gly 65 70 80	240
tac gcg gga ccg cag gga gag tac atc gtg gta ctc gaa gac acg ctg Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val 90 Val Leu Glu Asp Thr Leu 85 95	288
gcc gtt cac aac gtg atc gtg tgt acg caa tgc tcg tgt act gcg tgg Ala Val His Asn Val Ile Val Cys Thr 105 Gln Cys Ser Cys Thr Ala Trp 100 110	336
ccc gtg ctg ggg ctg ccg ccc gat tgg tac aag agt ccg gag tat cgc Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser 125 Pro Glu Tyr Arg 115 120	384
gcc cgc gtc gtg cgg gag ccg cga cgg gtg ctt cgc gaa atg ggc ctc Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg 140 Glu Met Gly Leu 130 135	432
gag cta tcc gag agc gtg acg atc cgc gtg tgg gat acg act gcg gaa Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu 145 150 155 160	480

acg cgc ttc ctg gtg ctg ccg ctt cgg ccg gcg gga acc gaa ggg tgg	528
Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp	
165 170 175	
agc gcg gag cag ctc gcg tcg ctc gtc acg cgc gag gcg atg atc ggc	576
Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly	
180 185 190	
gtg gcg cgg gtc gag gtg gtg tag	600
Val Ala Arg Val Glu Val Val	
195	

<210> 52
 <211> 199
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M6dE2
 <400> 52

Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg	
1 5 10 15	
Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu	
20 25 30	
Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro	
35 40 45	
Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr	
50 55 60	
Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly	
65 70 75 80	
Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu	
85 90 95	
Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp	
100 105 110	
Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg	
115 120 125	
Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu	
130 135 140	
Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu	
145 150 155 160	
Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp	
165 170 175	
Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly	
180 185 190	

val Ala Arg val Glu val val
195

<210> 53
<211> 645
<212> DNA
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M25A18

<220>
<221> CDS
<222> (1)..(645)

<400> 53

atg agc ggc acg cat cac cac gac cat gac cac gat cat gac cat gcc	48
Met Ser Gly Thr His His His Asp His Asp His Asp His Ala	
1 5 10 15	
cat ccg ggc gtc gcc aag gac gag aag gtc cac ggc tat tac caa ttg	96
His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu	
20 25 30	
ctc ggc ctc gcc atc aaa gag ctg ctg atc gaa aaa ggc gtc atc acc	144
Leu Gly Leu Ala Ile Lys Glu Leu Ile Glu Lys Gly Val Ile Thr	
35 40 45	
gcc gcc gag gtg cgc caa gcg atc gag gcg cgc gac gcg atc acg ccg	192
Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro	
50 55 60	
tgc ctc ggc ggc aag gtg gtc gcg cgc gcc tgg acc gat ccg gcc tac	240
Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr	
65 70 75 80	
aag gcg cgg ctg atc gcc gat ccc gcc gcc gcc atg atg gag atg ggc	288
Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Ala Met Met Glu Met Gly	
85 90 95	
gtc gat ctc ggc ccc acc gga ctc gcc atc gcc gag aac acg ccg gag	336
Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu	
100 105 110	
gcg cac aac gtc atc gtc tgc acc ctg tgc tgc tgc tat ccg cgc gcc	384
Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala	
115 120 125	
gtg ctc ggc ctg ccg ccc tcc tgg tac aag gac cgc gat tac cgg tcg	432
Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser	
130 135 140	
cgc gtg gtg cgc gag ccg cgc gcc gtg ctc aag gag ttc ggc acg gaa	480
Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu	
145 150 155 160	
ttg ccc gac gac gtc gac gtc cgc gtc cac gat tcg acc gcc gat ctg	528
Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu	
165 170 175	
cgc tat ctc gtg ctg ccg atg cgc ccg gcc ggc acc gag ggc atg agc	576
Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser	
180 185 190	
gag gcg gag ctg gcc gag atc gtg acg cgc gac tgc atg atc ggc gtg	624
Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val	
195 200 205	
acg gtg ccg aaa gcg ccc taa	645

Thr Val Pro Lys Ala Pro
210

<210> 54
<211> 214
<212> PRT
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M25A18
<400> 54

Met Ser Gly Thr His His His Asp His Asp His Asp His Asp His Ala
1 5 10 15

His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu
20 25 30

Leu Gly Leu Ala Ile Lys Glu Leu Leu Ile Glu Lys Gly Val Ile Thr
35 40 45

Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro
50 55 60

Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr
65 70 75 80

Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Ala Met Met Glu Met Gly
85 90 95

Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu
100 105 110

Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala
115 120 125

Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser
130 135 140

Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu
145 150 155 160

Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu
165 170 175

Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser
180 185 190

Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val
195 200 205

Thr Val Pro Lys Ala Pro
210

```

<210> 55
<211> 627
<212> DNA
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase

<220>
<221> CDS
<222> (1)..(627)

<400> 55

atg agc ggt cac cat cac gac cac gac cat gag cac gac aac cac ttc      48
Met Ser Gly His His His Asp His Asp His Glu His Asp Asn His Phe
1                               5                               10          15

acg ccg atc gaa gcg cgc gtg aag gcg ctg gaa tcg ctg ctg gtc gcc      96
Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala
20                          25                          30

aag ggc tat gtc gat ccc gcc gcg ctc gat gcg atc atc gac acc tat     144
Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr
35                          40                          45

gag acg aag atc ggc ccg cgc aac ggc gcc cgc gtc gtc gcc aag gcc     192
Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala
50                          55                          60

tgg acc gat ccg gaa ttc gcg gcg cgg ctc aag cag gat ggc agc gcc     240
Trp Thr Asp Pro Glu Phe Ala Ala Arg Leu Lys Gln Asp Gly Ser Ala
65                          70                          75      80

gcc gtc gcc gaa ctc ggc tat ggc ggg cgt ggc ggc gag cat atc gtc     288
Ala Val Ala Glu Leu Gly Tyr Gly Gly Arg Gly Gly Glu His Ile Val
85                          90                          95

gcc tgt ttc aat acg ccc gaa gag cac aac ctg atc gtc tgc acg ctc     336
Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu
100                         105                        110

tgc tcg tgc tat ccc tgg ccg gtg ctc ggc ctg ccg ccg gtc tgg tac     384
Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr
115                        120                        125

aaa tcc ccg ccc tat cgc tcg aaa gcg gtg atc gac ccg cgc ggc gtg     432
Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val
130                        135                        140

ctg gcc gat ttc ggc gtg acc ctg ccg gag gga caa agg atc cgc gtc     480
Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val
145                        150                        155      160

tgg gat tcc acc gcc gaa acc cgc ttc att gtc atc ccc ctg cgc ccg     528
Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro
165                        170                        175

gcc ggg acg gaa ggc tgg tcg gaa gaa cag ctg gcg gcg atc gtg acg     576
Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr
180                        185                        190

cgt gac agc atg atc ggc acc ggc gtg gtc agc gcg gag gct tcg cga     624
Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg
195                        200                        205

tga                                                                    627

```

<210> 56
 <211> 208
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase

<400> 56

```

Met Ser Gly His His His Asp His Asp His Glu His Asp Asn His Phe
1          5          10          15

Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala
          20          25          30

Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr
          35          40          45

Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala
          50          55          60

Trp Thr Asp Pro Glu Phe Ala Ala Arg Leu Lys Gln Asp Gly Ser Ala
65          70          75          80

Ala Val Ala Glu Leu Gly Tyr Gly Gly Arg Gly Gly Glu His Ile Val
          85          90          95

Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu
          100          105          110

Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr
          115          120          125

Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val
          130          135          140

Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val
145          150          155          160

Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro
          165          170          175

Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr
          180          185          190

Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg
          195          200          205

```

<210> 57
 <211> 696
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M3aG10

<220>
 <221> CDS
 <222> (1)..(696)

<400> 57

atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc	48
Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr	
1 5 10 15	
ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac	96
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His	
20 25 30	
cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc	144
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu	
35 40 45	
gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac	192
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp	
50 55 60	
gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg	240
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala	
65 70 75 80	
cgc gtt gtc gcg cgg gcc tgg gtt gac ccg gac tac aag caa cgg tta	288
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu	
85 90 95	
ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg	336
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser	
100 105 110	
cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac	384
Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn	
115 120 125	
ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc	432
Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly	
130 135 140	
ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg	480
Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val	
145 150 155 160	
atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac	528
Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp	
165 170 175	
cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta	576
His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu	
180 185 190	
gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg	624
Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala	
195 200 205	
ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc	672
Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val	
210 215 220	

gcg ccg ccg gga ggc cgc gga tga
 Ala Pro Pro Gly Gly Arg Gly
 225 230

696

<210> 58
 <211> 231
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M3aG10

<400> 58

Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr val Ala Leu Thr
 1 5 10 15

Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His
 20 25 30

Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg val Lys Ser Leu
 35 40 45

Glu Ser Leu Leu val Glu Lys Gly Leu val Glu Arg Ala Ala Leu Asp
 50 55 60

Ala Leu val Asp Thr Tyr Glu His Lys val Gly Pro Arg Asn Gly Ala
 65 70 75 80

Arg val val Ala Arg Ala Trp val Asp Pro Asp Tyr Lys Gln Arg Leu
 85 90 95

Phe Ala Asn Gly Thr Ala Ala val Ala Glu Phe Gly Tyr Ser Gly Ser
 100 105 110

Gln Gly Ala Asp Ile Arg val val Glu Asn Thr Ala Thr val His Asn
 115 120 125

Leu val val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro val Leu Gly
 130 135 140

Leu Pro Pro val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg val val
 145 150 155 160

Ile Asp Pro Arg Gly val Leu Arg Glu Phe Gly val val Leu Pro Asp
 165 170 175

His Ile Glu val Arg val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
 180 185 190

val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
 195 200 205

Leu Ala Leu Leu val Thr Arg Asp Ala Met Ile Gly val Ala Lys val
 210 215 220

Ala Pro Pro Gly Gly Arg Gly
225 230

<210> 59
<211> 609
<212> DNA
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M73dC9

<220>
<221> CDS
<222> (1)..(609)

<400> 59

atg agc tgc aag ccc acc gaa gat ctc ggc acc tac cag ccg ctc acc	48
Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr	
1 5 10 15	
tac tac cag atg atg gaa gtg agc ctg cgc gag ctg ctg gtg gag aag	96
Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys	
20 25 30	
ggc gtg atc acc gaa gcg gaa gtc gcc cgc gcg atg ggc gag atc ggc	144
Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly	
35 40 45	
gcg aga agc ccg gag gcg ggc gcg aag atg gtc gcg cgc gcg tgg gtg	192
Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val	
50 55 60	
gac ccg gcg tac aag gcg cgc atg ctt gcc gac ggc agc aag gcc gcc	240
Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala	
65 70 75 80	
gag gag ctc ggg ttc gag gtg ccg ggc ctc aag ctg atc gtg gtc gag	288
Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu	
85 90 95	
aac acc gcg gac acg cac aac gtg gtc gtg tgc acg ctg tgc tcg tgc	336
Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys	
100 105 110	
tac ccg cgc atc ctg ctc ggc atc ccg ccc gag tgg tac aag tcg cgc	384
Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg	
115 120 125	
agc tac cgc agc cgc aca gtg cgc gag ccg cgc gcg gtg ctc gcc gaa	432
Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu	
130 135 140	
ttc ggc acg acc atc ccg gag aac gtc gcg atc cga gtg cac gac agc	480
Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser	
145 150 155 160	
act gcg gac atg cgc tac ctc gtg atg ccg atg cgc cct gcg ggc acc	528
Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr	
165 170 175	
gaa aat ttc acc gaa gag cag ctc gct gca ttg gtg acg cgc gac agc	576
Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser	
180 185 190	
ctg atc ggt gtt tcc tta gca acg ctt ccg tag	609
Leu Ile Gly Val Ser Leu Ala Thr Leu Pro	
195 200	

<210> 60
 <211> 202
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - alpha unit nitrile hydratase - M73dC9

<400> 60

Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr
 1 5 10 15

Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys
 20 25 30

Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly
 35 40 45

Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val
 50 55 60

Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala
 65 70 75 80

Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu
 85 90 95

Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys
 100 105 110

Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg
 115 120 125

Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu
 130 135 140

Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser
 145 150 155 160

Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr
 165 170 175

Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser
 180 185 190

Leu Ile Gly Val Ser Leu Ala Thr Leu Pro
 195 200

<210> 61
 <211> 825
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase

<220>
 <221> CDS
 <222> (1)..(825)

<400> 61

atg gtg gga cgt ggg aag tgg gca ctt ggc agt agg cag ttt gct gcg Met Val Gly Arg Gly Lys Trp Ala Leu Gly Ser Arg Gln Phe Ala Ala 1 5 10 15	48
gct gcc aac tgg caa ctt atc agt cgc cct tca tgg tca gct tgt aat Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn 20 25 30	96
ata ttg gtc ctc atg agc gcc acg cac ccc aaa aag cgc gcc gcc gac Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp 35 40 45	144
atc ggc ggc aac aaa gcc ggc gcg gtg gac acc gcg gat cac ggc atg Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met 50 55 60	192
aag ttc tgg gag cgg cag gcc aac gcc ctg cgc acc gcg ctg cgg cgc Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg 65 70 75 80	240
aat gga ctg atg agc gta gat gag ctg cgc cgc gca gcg gag gac ctg Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu 85 90 95	288
gga gac cgc tac gcg aag ctt gag tac ttc gag cgc acg acg ttc gcg Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala 100 105 110	336
ctg cgc acg gtc ctg ctc gaa aag ggc tac ttc acg gag gag tcg ctc Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu 115 120 125	384
gcg gcg aag atg gcc gag gtg cgg aag ccg ctt cga tgt gcc gcg caa Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln 130 135 140	432
gaa gga att gcc ggt gaa gaa gaa agt gaa gcg atg aac cca gcg acg Glu Gly Ile Ala Gly Glu Glu Glu Ser Glu Ala Met Asn Pro Ala Thr 145 150 155 160	480
ggc aag cag gac ggc caa cgg ctg cca tct acg tat acc gcg gcg ccc Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro 165 170 175	528
ggg cac cga ttc gat gtc ggt gac cgc gtt gtg gtc aag cgc tca aat Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn 180 185 190	576
ccg ccc ggc cac cgc cgc acg cct cat tac atc cgc ggc aag acg ggc Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly 195 200 205	624
gtg atc gag cgc atc tgc ggc gcc ttc ccc aac ccg gaa gag ctg gca Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala 210 215 220	672

tac gga ttc gac ggc gaa ccg aag aag gtg ctc tac cgc gtg cga ttc	720
Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe	
225 230 235 240	
cgg caa aaa gag gtg tgg ccg gcc tat cgc ggc ccg gcg cac gac gtg	768
Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val	
245 250 255	
atc gag atg gag att ttc gag cat tgg ctc gag ccg gcg cag agc cag	816
Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln	
260 265 270	
aaa acc tga	825
Lys Thr	

<210> 62
 <211> 274
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase

<400> 62

Met Val Gly Arg Gly Lys Trp Ala Leu Gly Ser Arg Gln Phe Ala Ala	
1 5 10 15	
Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn	
20 25 30	
Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp	
35 40 45	
Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met	
50 55 60	
Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg	
65 70 75 80	
Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu	
85 90 95	
Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala	
100 105 110	
Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu	
115 120 125	
Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln	
130 135 140	
Glu Gly Ile Ala Gly Glu Glu Glu Ser Glu Ala Met Asn Pro Ala Thr	
145 150 155 160	
Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro	
165 170 175	

Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn
180 185 190

Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly
195 200 205

Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala
210 215 220

Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe
225 230 235 240

Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val
245 250 255

Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln
260 265 270

Lys Thr

<210> 63
<211> 627
<212> DNA
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M12K24

<220>
<221> CDS
<222> (1)..(627)

<400> 63

atg gac ggc atg cac gac ctg gga ggc agg cag ggc ttc gga ccg gtt Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val 1 5 10 15	48
cgc tac acg atc gac gcg ccc gca ttc cat tcg ccg tgg gaa gtg cgc Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg 20 25 30	96
gcg aat tcg ctc tat gcg ttc gcg gtg cgc ctc ggc atc ttc aac atg Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met 35 40 45	144
gac gaa tac cgc cat gcg atc gag cgg atg gag ccg cgc cat tac ctc Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu 50 55 60	192
ggc gcc ggc tat tac gaa cgc tcg ttg acc ggc ctc gcg acc ttg ctg Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu 65 70 75 80	240
gtc gag aag ggc gtc gtg acg cgc gag gaa ctc gag acc cgg gcg cag Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln 85 90 95	288
ggc cgc tac ccg ctg gcg atg ccc agc gcg cct ggc cgc acc aat gcg Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala 100 105 110	336

cag gca cgc gag cgt ttc cag ccg ggc gac cgg gtt cgc gtc aag gcg Gln Ala Arg 115 Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala	384
gat ttc gtg tgc ggg cac gtg cgg atg ccg gcg tac atc cgc ggc aag Asp Phe Val 130 Ser Gly His Val 135 Arg Met Pro Ala Tyr 140 Ile Arg Gly Lys	432
acc ggc gtg gtc gtc agc gag tcc ccg gac tat ccg ttt ccc gat gcg Thr Gly Val 145 Val Val Ser 150 Glu Ser Pro Asp Tyr 155 Pro Phe Pro Asp Ala 160	480
cat gcg cac tgc gtc gat gcc cag gac gag cca acc tac gac gtg cgc His Ala His 165 Ser Val 165 Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val 175 Arg	528
ttc cgc agc gag gat cta tgg ccg gat tcc gcc gat tcc gca ctc gtt Phe Arg Ser 180 Glu Asp Leu Trp Pro Asp 185 Ser Ala Asp Ser Ala 190 Leu Val	576
cac gtc ggc gta ttc cag agc tac ctc gag cgg gag tcg acg cca gga His Val 195 Gly Val Phe Gln Ser Tyr 200 Leu Glu Arg Glu Ser 205 Thr Pro Gly	624
tag	627

<210> 64
 <211> 208
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M12K24
 <400> 64

Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro val 1 5 10 15
Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu val Arg 20 25 30
Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met 35 40 45
Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu 50 55 60
Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu 65 70 75 80
Val Glu Lys Gly val val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln 85 90 95
Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala 100 105 110
Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg val Lys Ala 115 120 125
Asp Phe val Ser Gly His val Arg Met Pro Ala Tyr Ile Arg Gly Lys 130 135 140

Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala
145 150 155 160

His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg
165 170 175

Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val
180 185 190

His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly
195 200 205

<210> 65

<211> 660

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M29M24

<220>

<221> CDS

<222> (1)..(660)

<400> 65

atg aac ggc gtt cat gac atg ggc ggc atg cac ggc atg ggt gcg atc 48
Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile
1 5 10 15

cgc cgc gag gag aac gag ccc gct ttc cac gag ccc tgg gag ggg cgg 96
Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg
20 25 30

gtt ttc gct ctg acc acg gcg gtc gag gcc tgg ggt cgg tgg acc ctc 144
Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu
35 40 45

gat gct tcc cga cac cgg atc gag cgg atg aat gcg gcg gac tat ctg 192
Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu
50 55 60

cgg gtg agc tat tac gag aag tgg ctc gag tcg ctt ctc gct ctc ctg 240
Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu
65 70 75 80

tcc gag acc gga atg gcg agt ccg gcg gag ata cgg agt ggg gag cgt 288
Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg
85 90 95

gcc gac ggc aca ccg aaa gcg acc ccg ccg ctc ccg gcc gac cac gtg 336
Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val
100 105 110

acg gcg att ctc gcc agc ggg ttt ccc gcg agc cgg gag gcg gga gct 384
Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala
115 120 125

gcg cct cgc ttc cga gtg agc gag cgg gtg cgc acc cgg aac atc aac 432
Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn
130 135 140

ccg acg act cac acg cgc ctt ccg cga tac gcc cgg cgg aag ctc ggg 480
Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly
145 150 155 160

acg atc gag cgc gac cac gga gtg ttc gtc ttc ccg gat acg aac gcg Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala	528
165 170 175	
cac gct ctc ggg gag aaa ccg cag cac gtc tat tcg gtt cgt ttc gag His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu	576
180 185 190	
gcg cgt gag ctc tgg ggc gag act gcc agg cca gag gat tcc gtc tac Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr	624
195 200 205	
atc gat ctt tgg gac gag tac ctt gaa ccc gtg tag Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val	660
210 215	

<210> 66
 <211> 219
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M29M24
 <400> 66

Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile 1 5 10 15
Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg 20 25 30
Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu 35 40 45
Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu 50 55 60
Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu 65 70 75 80
Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg 85 90 95
Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val 100 105 110
Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala 115 120 125
Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn 130 135 140
Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly 145 150 155 160
Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala 165 170 175

His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu
180 185 190

Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr
195 200 205

Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val
210 215

<210> 67
<211> 660
<212> DNA
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M2K17

<220>
<221> CDS
<222> (1)..(660)

<400> 67

atg acc aat tcg ctg cac gac atg ggc ggc atg cac ggc ttt ggc cgg 48
Met Thr Asn Ser Leu His Asp Met Gly Gly Met His Gly Phe Gly Arg
1 5 10 15

gtc gag ccc gag ccg aac gag ccg ccg ttt cac cag cgc tgg gag ggc 96
Val Glu Pro Glu Pro Asn Glu Pro Pro Phe His Gln Arg Trp Glu Gly
20 25 30

cgg gtg ctg ggg atg cag cgc gcc atg ggc ttt acc ggg ctg tgg acc 144
Arg Val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr
35 40 45

atc gac gcc ggc cgc gcc tcg ctc gaa gcc ctg ccg cca tta gcg tat 192
Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr
50 55 60

ctg ggt tcg tcc tac tat cgg cgc tgg ttt ctt ggc ctg gag agc cgg 240
Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg
65 70 75 80

ctg ctg ctg cgc ggc ctc gtt ggc gag gac gag atc gcg gca ggc cgt 288
Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg
85 90 95

tcg atg cgc gcc ggc gcc atg ttg ccg cgc acc ctg acc cag gcc gat 336
Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp
100 105 110

gtg gag aaa acc ctg acc cgc ggc gac ttc gcc cgc ccg acc aac acc 384
Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr
115 120 125

ccg gcg cgt ttc cag ccg ggc gac ccg gtg caa acg aag aac atc aac 432
Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn
130 135 140

ccg gcg acc cac acc cgc ctg ccg cgc tat gcc cgc ggc aag act ggc 480
Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly
145 150 155 160

acg gtc gag gcg gtc cgc ggc gtt cac gtc ttt ccc gac acc gcc gcg 528
Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala
165 170 175

ctc ggc gcc ggc gac gac ccg caa tgg ctc tac gcc gtg gtc ttc ccg 576
 Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val val Phe Pro
 180 185 190

gcg cgc gag ttg tgg gga gag gcg gcc gat ccc gcg atc aaa atc tcg 624
 Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser
 195 200 205

atc gag gcg ttc gaa ccc tat atc gac ccc gca tga 660
 Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala
 210 215

<210> 68
 <211> 219
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M2K17
 <400> 68

Met Thr Asn Ser Leu His Asp Met Gly Gly Met His Gly Phe Gly Arg
 1 5 10 15

val Glu Pro Glu Pro Asn Glu Pro Pro Phe His Gln Arg Trp Glu Gly
 20 25 30

Arg val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr
 35 40 45

Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr
 50 55 60

Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg
 65 70 75 80

Leu Leu Leu Arg Gly Leu val Gly Glu Asp Glu Ile Ala Ala Gly Arg
 85 90 95

Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp
 100 105 110

val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr
 115 120 125

Pro Ala Arg Phe Gln Pro Gly Asp Arg val Gln Thr Lys Asn Ile Asn
 130 135 140

Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly
 145 150 155 160

Thr val Glu Ala val Arg Gly val His val Phe Pro Asp Thr Ala Ala
 165 170 175

Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala val val Phe Pro
 180 185 190

Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser
 195 200 205

Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala
 210 215

<210> 69
 <211> 663
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M23dA12

<220>
 <221> CDS
 <222> (1)..(663)

<400> 69

atg gac ggc gtg cac gac atg ggc ggc atg cac ggt ttc ggc aag gtc Met Asp Gly Val His Asp Met Gly Gly Met His Gly Phe Gly Lys Val 1 5 10 15	48
gag ccg gaa gcg aac gag ccc gcc ttc cat gcg gaa tgg gaa ggc cgc Glu Pro Glu Ala Asn Glu Pro Ala Phe His Ala Glu Trp Glu Gly Arg 20 25 30	96
tgc ctc gcg ctc aac cgc gcc atg ggt gcg atc ggc gcc tgg acc atc Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile 35 40 45	144
gat gaa ggc cgt gcc ggc atc gag atc ctg ccg ccg gag att tat ctt Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu 50 55 60	192
ggc agt tcg tac tat gga aaa tgg gcg cgg cgg ctg gag aat atg gtg Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val 65 70 75 80	240
gtc gca cgc ggg ttc gcg ggc gcc gat gaa ctc gcc gcg ggt cgc gca Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala 85 90 95	288
gcg cgt ccc ggc aga tcg gtg aaa cga aag ctt acg gtc gcc gaa gtg Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val 100 105 110	336
ccg cgc acg ctg acg cgc ggt tca ttt ttc cgc gag gca aca aag ccg Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro 115 120 125	384
gca cga ttt gcg gtc ggc gaa cgc gtg cgc acc agg aac att cat ccg Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro 130 135 140	432
gcg acg cac act cgg ttg ccg cga tat gcg cgc ggc cat gtc ggc gtg Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val 145 150 155 160	480
atc gag gcg atc cgc ggt tgc cac gta ttt ccc gac tcg gtt gcg atc Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile 165 170 175	528
ggc gcc ggc gag aac ccg caa tgg ctt tat acg gtg gtg ttc gaa ggc Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly 180 185 190	576

Cgc acg ctg tgg ggc gat agc gcc gat ccg acg ctt aag gtc tcg atc 624
Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile
195 200 205

<210>	70
<211>	220
<212>	PRT
<213>	Unknown

Met Asp Gly Val His Asp Met Gly Gly Met His Gly Phe Gly Lys Val
1 5 10 15

Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile
35 40 45

Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val
65 70 75 80

Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val
100 105 110

Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro
130 135 140

Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile
165 170 175

Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile
195 200 205

Glu Ala Phe Glu Pro Tyr Leu Glu Pro Ala Gln Pro
 210 215 220

<210> 71
 <211> 888
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M49bD9

<220>
 <221> CDS
 <222> (1)..(888)

<400> 71

atg aac ggc gta cac gat ctt ggc ggg atg gat ggt ttc ggc cgg gtg Met Asn Gly Val His Asp Leu Gly Gly Met Asp Gly Phe Gly Arg Val 1 5 10 15	48
atg gcg gag gcg gac gag ccg gtc ttt cat gag ccc tgg gaa ggt cgc Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg 20 25 30	96
gtg ttt gcg ctc aac atg ctc ggc atc ggg cgc gag ccc att ccg gtg Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val 35 40 45	144
gac gcg ctg cgc cat cgc att gag cgg atc gag ccg tgg cgc tat ctg Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu 50 55 60	192
acg tcg agc tat tac gaa cga tgg ctg gcc gaa atg gag cag gcc atc Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile 65 70 75 80	240
atc gat gcg ggc acg ctg act cct ggt gaa atc gat gcg cga atg ggc Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly 85 90 95	288
gag ctc gaa acg gat cct gat cgc cca ctg cca agg act gat aac cct Glu Leu Glu Thr Asp Pro Asp Arg Pro Leu Pro Arg Thr Asp Asn Pro 100 105 110	336
gag cat gcc gat ggg gtg gcg gcg gcg ttg cgc gcc ggc agt ccc gta Glu His Ala Asp Gly Val Ala Ala Leu Arg Ala Gly Ser Pro Val 115 120 125	384
acg cgc aag att cgc aag cag ccg cgc ttc aca atc ggc gat cgg gtc Thr Arg Lys Ile Arg Lys Gln Pro Arg Phe Thr Ile Gly Asp Arg Val 130 135 140	432
gta acg cgc aat ctt aat ccg cac ggc cat acg cgg ctg ccg cgc tat Val Thr Arg Asn Leu Asn Pro His Gly His Thr Arg Leu Pro Arg Tyr 145 150 155 160	480
gcg cgc ggc aag cgc ggc gtc gta acg ctg cac cat ggc gca cat gtc Ala Arg Gly Lys Arg Gly Val Val Thr Leu His His Gly Ala His Val 165 170 175	528
ttt ccg gat acg aac gcg cac ggg ctg ggc gag cat ccg cag cat ctc Phe Pro Asp Thr Asn Ala His Gly Leu Gly Glu His Pro Gln His Leu 180 185 190	576
tat acg gtg cga ttt cct gcg cgc gag tta tgg agc gac gcg gcc gag Tyr Thr Val Arg Phe Pro Ala Arg Glu Leu Trp Ser Asp Ala Ala Glu 195 200 205	624

ccg aaa gaa tcg ata atg atc gat ttg tgg gag agc tat ctt caa ccc Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro 210 215 220	672
gat atc ggc agc aaa gcg tcg tcg tcc gcg aaa ggc aaa gcg acg ccg Asp Ile Gly Ser Lys Ala Ser Ser Ser Ala Lys Gly Lys Ala Thr Pro 225 230 235 240	720
aaa gtt aag ccc gca atg gcc aag gca acc gcc aag gta agc gtc tcg Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser 245 250 255	768
gcc aag gcc aaa act cgg gga aag gcg gcg ccg aag gag cgt cca aaa Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys 260 265 270	816
ctg aaa cct gcg cga gcg gcg acc tca gca gca tcc ggc ggc gaa aaa Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys 275 280 285	864
gct aag cga aag gcc aaa cga tga Ala Lys Arg Lys Ala Lys Arg 290 295	888

<210> 72
<211> 295
<212> PRT
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M49bD9

<400> 72

Met Asn Gly Val His Asp Leu Gly Gly Met Asp Gly Phe Gly Arg Val 1 5 10 15
Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg 20 25 30
Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val 35 40 45
Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu 50 55 60
Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile 65 70 75 80
Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly 85 90 95
Glu Leu Glu Thr Asp Pro Asp Arg Pro Leu Pro Arg Thr Asp Asn Pro 100 105 110
Glu His Ala Asp Gly Val Ala Ala Ala Leu Arg Ala Gly Ser Pro Val 115 120 125
Thr Arg Lys Ile Arg Lys Gln Pro Arg Phe Thr Ile Gly Asp Arg Val 130 135 140

Val Thr Arg Asn Leu Asn Pro His Gly His Thr Arg Leu Pro Arg Tyr
 145 150 155 160
 Ala Arg Gly Lys Arg Gly Val Val Thr Leu His His Gly Ala His Val
 165 170 175
 Phe Pro Asp Thr Asn Ala His Gly Leu Gly Glu His Pro Gln His Leu
 180 185 190
 Tyr Thr Val Arg Phe Pro Ala Arg Glu Leu Trp Ser Asp Ala Ala Glu
 195 200 205
 Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro
 210 215 220
 Asp Ile Gly Ser Lys Ala Ser Ser Ser Ala Lys Gly Lys Ala Thr Pro
 225 230 235 240
 Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser
 245 250 255
 Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys
 260 265 270
 Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys
 275 280 285
 Ala Lys Arg Lys Ala Lys Arg
 290 295

<210> 73
 <211> 630
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M6dE2

<220>
 <221> CDS
 <222> (1)..(630)

<400> 73

atg gac ggc att cat gat ctc ggt ggg atg agc ggg ttc ggt ctc gtg Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val 1 5 10 15	48
gag atc gag ccc gat gag ccg gtg ttc cac gag ccc tgg gag gcg ctg Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu 20 25 30	96
gtt ttc gct ctg atg act ctc ggt atc ggg aag ctc ggc gcg tac aac Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn 35 40 45	144
gcc gat gag tac cgc cac tcg atc gag cgg atg gat ccg gcc cac tac Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr 50 55 60	192

ctt gcg gcg acg tac tac gag cgc atg ctc acc ggc gtc gca acg ctc Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu 65 70 75 80	240
ctc gtc gag aag aac gtc gtt gcc cgc gac gag ctc gaa gcg cgc gcc Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala 85 90 95	288
ggc ggg ccc ttc ccg ctg tca cgg ccg gtg gcc gag cgg ccg acg gcg Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala 100 105 110	336
gac ctt cgg ccc cag cca caa cca cgc ttc gcg gtc ggg gat cgg gtc Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val 115 120 125	384
gtc gtg cgc gac atc cac ccg gcc ggg cat act cgt gtg ccg cgc tac Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr 130 135 140	432
gtg cgg ggc aag cgc ggg acc gtc gtg cac gtc gcg ccg aaa ttc tcg Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser 145 150 155 160	480
ttc ccc gac acg gcc gcg cac ggg ctg acc cat cgg agc gag cac acg Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr 165 170 175	528
tat cac gtg gaa ttc gtc gcg agt gac ctt tgg gcc gac gtg gcc ggg Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly 180 185 190	576
agc aat gag agc gta ctc gtg gac ctg tgg gac ggc tat ctg gag ggc Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly 195 200 205	624
gca tga Ala	630

<210> 74
 <211> 209
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M6dE2
 <400> 74

Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val 1 5 10 15
Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu 20 25 30
Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn 35 40 45
Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr 50 55 60
Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu 65 70 75 80

Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala
 85 90 95
 Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala
 100 105 110
 Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val
 115 120 125
 Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr
 130 135 140
 Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser
 145 150 155 160
 Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr
 165 170 175
 Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly
 180 185 190
 Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly
 195 200 205

Ala

<210> 75

<211> 651

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M25A18

<220>

<221> CDS

<222> (1)..(651)

<400> 75

atg cgc ggc acg cac gat ctc ggc gga ttg ccc gcc ggc ccg gtg gac	48
Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp	
1 5 10 15	
acc gct ccc cac gaa ccg acc ttc tgg gaa aag cag gtg gac gcg atc	96
Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile	
20 25 30	
cac ggc ctg ctc ggc gat tcc aag cgc cgc atc acg ctg cgc gac gag	144
His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu	
35 40 45	
aac cgc ctc tat atc gaa tcg ctc ggc gac gac gtc tac aac acg ctc	192
Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu	
50 55 60	
ggc tat tac gag cgc tgg acc gcc gcc atg tgc cgc cag ctc atc gac	240
Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp	
65 70 75 80	

aag ggc gtg ctg acg cag gac gag atc gac gcc aag atc gcc gag ctg Lys Gly Val Leu Thr 85 Gln Asp Glu Ile Asp 90 Ala Lys Ile Ala Glu 95 Leu	288
cgc gcc cgc ggc gtc ggc gcg gga cga cga cga aac ggc ctg caa acc Arg Ala Arg Gly 100 Val Gly Ala Gly Arg 105 Arg Arg Asn Gly 110 Leu Gln Thr	336
gtg agc gcc gat ctg gcc gcc gat ctg gcc atc gcg ccg cgc ttc gcc Val Ser 115 Asp Leu Ala Ala Asp 120 Leu Ala Ile Ala Pro 125 Arg Phe Ala	384
gcc ggc gac cgc gtg cgg gtg cgc gac gat tat ccg ccc ggg cac atc Ala Gly 130 Asp Arg Val Arg Val 135 Arg Asp Asp Tyr Pro 140 Pro Gly His Ile	432
cgc acg ccg gtc tat gtg cgc ggc aag acg ggc gtg gtg acg cgc tgc Arg Thr 145 Pro Val Tyr Val 150 Arg Gly Lys Thr Gly 155 Val Val Thr Arg Cys 160	480
ttc ggc gcg ttc aag aac ccg gaa ttg ctc gcc atc ggc aag gac ggc Phe Gly Ala Phe 165 Lys Asn Pro Glu Leu 170 Leu Ala Ile Gly Lys 175 Asp Gly	528
ctg ccc aag aaa att ctc tac gaa gtg cgc ttc aag cag acc gat ctc Leu Pro Lys 180 Ile Leu Tyr Glu Val 185 Arg Phe Lys Gln Thr 190 Asp Leu	576
tgg ccc gac tat gcc ggg ccg gcg acc gat acg ctg ctg atc gac atc Trp Pro 195 Asp Tyr Ala Gly Pro 200 Thr Asp Thr Leu 205 Leu Ile Asp Ile	624
tac gaa cat tgg ctg agc gac gcg tga Tyr Glu 210 His Trp Leu Ser 215 Asp Ala	651
<210> 76	
<211> 216	
<212> PRT	
<213> Unknown	
<220>	
<223> Metagenome - beta unit nitrile hydratase - M25A18	
<400> 76	
Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp 1 5 10 15	
Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile 20 25 30	
His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu 35 40 45	
Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu 50 55 60	
Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp 65 70 75 80	
Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu 85 90 95	

Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr
100 105 110

Val Ser Ala Asp Leu Ala Ala Asp Leu Ala Ile Ala pro Arg Phe Ala
115 120 125

Ala Gly Asp Arg Val Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile
130 135 140

Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys
145 150 155 160

Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly
165 170 175

Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu
180 185 190

Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile
195 200 205

Tyr Glu His Trp Leu Ser Asp Ala
210 215

<210> 77
<211> 657
<212> DNA
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M50bd9

<220>
<221> CDS
<222> (1)..(657)

<400> 77

atg aac ggc atg cat gac atg ggc ggc atg cac ggc atg gga ccc att Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile 1 5 10 15	48
cag atc gag aag gac gag tgc ccc ttc cat gcg cgc tgg gaa ggc cgg Gln Ile Glu Lys Asp Glu Ser Pro phe His Ala Arg Trp Glu Gly Arg 20 25 30	96
gcg caa gcg atg tac aac gcc att gcg gcc acg ggc aga ctg gtg ctt Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu 35 40 45	144
ggc ggt aga ccc aca cgg gaa ggg ttc ccg ccg gcc gaa tat ctc cgc Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg 50 55 60	192
atg agc tac tat gaa ttg ggt ttc agg gtg ctg gtc gag gac ttg gtc Met Ser Tyr Tyr Glu Leu Gly phe Arg Val Leu Val Glu Asp Leu val 65 70 75 80	240
ctg aac ggt ttg gtg acg cgc gcg gaa atc acg agc ggc cgt ccg gca Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala 85 90 95	288

aag ggg gct gca aag tcg acg ccc gca atc acc gcc gcc acc gcg cag 336
Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln
100 105 110
gca tat atg ttc gcg ctc aaa tcg acc cgg cga gac gta ccg gtc acg 384
Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr
115 120 125
gcg cgt ttc caa gtc ggt cag cgt gtg cgc gcg cgc aac atc aat ccg 432
Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro
130 135 140
gtc acc cat acg cgc ctg ccc cgt tac gcg cgc ggc aaa ttc ggc gtt 480
Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val
145 150 155 160
atc gaa cgt gac cac ggt gtt tac agg ttc gac gat tcc ttt gcc acg 528
Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr
165 170 175
tcc ggc gac gag aag ccc cag cac gtt tat tct gtg cgc ttc gcg gcg 576
Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala
180 185 190
cgc gaa cta tgg ggc gaa gcc gcg ccg ccg cga gat gct gtc tat atc 624
Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile
195 200 205
gaa atc tgg gat gac aac ctt gag cca gcg tga 657
Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala
210 215

<210> 78
<211> 218
<212> PRT
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M50bD9

<400> 78

Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile
1 5 10 15

Gln Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg
20 25 30

Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu
35 40 45

Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg
50 55 60

Met Ser Tyr Tyr Glu Leu Gly Phe Arg Val Leu Val Glu Asp Leu Val
65 70 75 80

Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala
85 90 95

Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln
100 105 110

Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr
115 120 125

Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro
130 135 140

Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val
145 150 155 160

Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr
165 170 175

Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala
180 185 190

Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile
195 200 205

Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala
210 215

<210> 79
<211> 696
<212> DNA
<213> Unknown

<220>
<223> Metagenome - beta unit nitrile hydratase - M3aG10

<220>
<221> CDS
<222> (1)..(696)

<400> 79

atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr 1 5 10 15	48
ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His 20 25 30	96
cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu 35 40 45	144
gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp 50 55 60	192
gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala 65 70 75 80	240
cgc gtt gtc gcg cgg gcc tgg gtt gac ccg gac tac aag caa cgg tta Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu 85 90 95	288
ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser 100 105 110	336

cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn	384
ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly	432
ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val	480
atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp	528
cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu	576
gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala	624
ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val	672
gcg ccg ccg gga ggc cgc gga tga Ala Pro Pro Gly Gly Arg Gly	696

<210> 80
 <211> 231
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - beta unit nitrile hydratase - M3aG10
 <400> 80

Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr 1 5 10 15
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His 20 25 30
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu 35 40 45
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp 50 55 60
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala 65 70 75 80
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu 85 90 95
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser 100 105 110

Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn
115 120 125

Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly
130 135 140

Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val
145 150 155 160

Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp
165 170 175

His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu
180 185 190

Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala
195 200 205

Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val
210 215 220

Ala Pro Pro Gly Gly Arg Gly
225 230

<210> 81
<211> 327
<212> DNA
<213> Unknown

<220>
<223> Metagenome - p12K unit

<220>
<221> CDS
<222> (1)..(327)

<400> 81

atg aaa gat agc ccg gtc ttt cgc gag ccg tgg gaa gcg cag gcg ttt Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe 1 5 10 15	48
gcg ttg gcg atc tcg ttg caa gac cgt ggc gtg ttc acg cga gac gaa Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu 20 25 30	96
tgg gcg gcg gca ctc ggc gat gaa atc aag aag gcg caa gct gcc ggc Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly 35 40 45	144
gat ccc gat acg ggc gag act tat tac cat cat tgg atg gca gcg ctc Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu 50 55 60	192
gaa cgg ctg att gca gcc aag ggt gtt gcc gat acg cag acg ctc gcg Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala 65 70 75 80	240
cgc aca cgc gac gcc tgg cag cac gcc tgt gcg cga acg ccg cat gcc Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly 85 90 95	288

gcg cca atc gag cta aga ccg gac gac ttc agg aat tga 327
 Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn
 100 105

<210> 82
 <211> 108
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - p12K unit

<400> 82

Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe
 1 5 10 15

Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu
 20 25 30

Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly
 35 40 45

Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu
 50 55 60

Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala
 65 70 75 80

Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly
 85 90 95

Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn
 100 105

<210> 83
 <211> 321
 <212> DNA
 <213> Unknown

<220>
 <223> Metagenome - p12K unit

<220>
 <221> CDS
 <222> (1)..(321)

<400> 83

atg aga aca gtt gct gag caa atc gcg gct gat ctt gcg agt ccg gcg 48
 Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala
 1 5 10 15

gcg att ccg cgc cgc aac ggc gag ccg gtc ttc gac gag cct tgg gaa 96
 Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu
 20 25 30

agt cgt gcg ttt ggg ata gcg gtc gcc ctt tcc gag ggt ggc ctc tat 144
 Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr
 35 40 45

tca tgg gat gaa ttt cgc gat tgc ctg att gct gaa atc aca gcg gcg	192
Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala	.
50 55 60	
gat gcg cgc ggc gag cat acg agc tat tac gaa cgg ttt ctc gcc gcc	240
Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala	
65 70 75 80	
ctg cag cat ctg ctc gcg gcc aaa cgc ctc tgc act ccc gat gaa gtc	288
Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val	
85 90 95	
gag cgg cgg atg aac act agc gca ggc acc tga	321
Glu Arg Arg Met Asn Thr Ser Ala Gly Thr	
100 105	

<210> 84
 <211> 106
 <212> PRT
 <213> Unknown

<220>
 <223> Metagenome - p12K unit

<400> 84

Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala	
1 5 10 15	
Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu	
20 25 30	
Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr	
35 40 45	
Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala	
50 55 60	
Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala	
65 70 75 80	
Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val	
85 90 95	
Glu Arg Arg Met Asn Thr Ser Ala Gly Thr	
100 105	


```

<210> 85
<211> 426
<212> DNA
<213> Unknown

<220>
<223> Metagenome - p12K unit

<220>
<221> CDS
<222> (1)..(426)

<400> 85

atg aca acc ttg agc cag cgt gaa gcg gcc ccc tcg gcc gag ctt ctt    48
Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu
1                               5                               10                               15

gac cta ccg caa ctt cca agc gac acc gac ggc ccc gtc ttc gcg gaa    96
Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu
20                               25                               30

cct tgg gaa gcg gaa gcg ttt gcg ctt gcc gta agt ctt tca gag caa   144
Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln
35                               40                               45

gga cat ttc acg tgg aag gaa tgg gca gca acg ctc gcc gat gaa ctg   192
Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu
50                               55                               60

gag ggc gcc gcc aat cgc ggc gag ccg gat gac ggt acg cat tat tat   240
Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr
65                               70                               75                               80

gag tac tgg ctg acg gcc ctg gaa agg ctg gtt acg atc aag ggc ctg   288
Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu
85                               90                               95

aca gat cag caa gcg atg cgc gag cgc aaa gag gcg tgg gaa gaa gcc   336
Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala
100                              105                              110

tat cgc cat acc ccg cat ggc gcg cca gtt gaa ctt atg tct ccg ctc   384
Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu
115                              120                              125

gat caa agc cgg ata gcc gaa gag gac agc gaa tcc tca tag         426
Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser
130                              135                              140

```

```

<210> 86
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Metagenome - p12K unit

<400> 86

Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu
1                               5                               10                               15

Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu
20                               25                               30

Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln
35                               40                               45

```

Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu
 50 55 60
 Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr
 65 70 75 80
 Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu
 85 90 95
 Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala
 100 105 110
 Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu
 115 120 125
 Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser
 130 135 140